

**IN THE TITLE:**

Please replace the existing title with the following title:

--POLYNUCLEOTIDES ENCODING POLYPEPTIDES FOR PHOSPHORYLATION  
AND CELL DIFFERENTIATION--

**IN THE SPECIFICATION:**

Please amend paragraph [0023] as follows:

-- Figure 1A depicts a sequence alignment of amino acid sequences (SEQ ID NOs: 2, 4, 6, 8 and 68) surrounding the catalytic domain and relation of SCP to FCP1.—

Please amend paragraph [0080] as follows:

-- The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (J. Mol. Biol. (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available on the world wide web at <http://www.gcg.com>), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available on the world wide web at [gcu.com](http://www.gcg.com)), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6.—

Please amend Table 1 at page 90, with the following Table 1:

**--Table 1**

Fly primers for qRT-PCR (SEQ ID NOs are in parenthesis)

Name of gene	5' sequence	3' sequence	Accession no.
SCP1	5' atggcgaactatacagactgcgttc 3' (18)	5' ctgtctgtgtggtaacatgg 3' (32)	CG5830
GAPDH	5' atcaacgacaactcgagatcg 3' (19)	5' gcggtggagtagccaaactcg 3' (33)	CG12055
ribosomal protein S35	5' atgtcgcttgc 3' (20)	5' ttataggatctcgatttcggc 3' (34)	CG5497
beta-actin	5' tgaagatcctcaccgagcg 3' (21)	5' gacggactcg 3' (35)	NM_079486
Na Channel II	5' cagctggcgggagtg 3' (22)	5' tgcgcagtcgc 3' (36)	CG9071
synapsin	5' gagctgtcg 3' (23)	5' cgctggattgggagaagg 3' (37)	CG3985
cholineAcetylTra nsferase	5' actggccattactactgg 3' (24)	5' ccgtaaacccgcgcattaa 3' (38)	CG32848
ELAV	5' caacgaagccgagcg 3' (25)	5' tggcatggcac 3' (39)	CG4396
beta-tubulin	5' gcaacaactggccaaagg 3' (26)	5' ctggcatcaacatcg 3' (40)	CG9277
Neurofilament H	5' gcctccaaggcac 3' (27)	5' cgatcagaatggatcg 3' (41)	CG7421
peptidyl-glycine oxygenase	5' ctgc 3' (28)	5' ccctggctgaagcagaactt 3' (42)	CG3832
myosin-light-chain-kinase	5' ctgcgc 3' (29)	5' tatggcataaaagg 3' (43)	CG1915
GCM	5' caacggactaacggc 3' (30)	5' gttctcgccatgttgc 3' (44)	CG12245
nMDAR	5' ctgcattgttctctgg 3' (31)	5' cgtatcgaggtagac 3' (45)	CG14793

**Mouse Primers for RT-PCR**

Name of gene	5' sequence	3' sequence	Accession no.
SCP1	5' cggccgtcattactcagatc 3' (46)	5' gcagtgaacagcacatcaa 3' (53)	AY028804
GAPDH	5' tccaccaccctgtgtgc 3' (47)	5' accacagtccatgc 3' (54)	NM_008084
ngn1	5' catctgtatctcgactgtcc 3' (48)	5' gggcagagatgtgtgc 3' (55)	NM_010896
beta-tubulin	5' tgcctcaccaggctctgc 3' (49)	5' cttaacatgtgtgc 3' (56)	NM_023716
stra13	5' ctgtggcatggggaaacatgtgc 3' (50)	5' agaaggccaggc 3' (57)	NM_016665
GAD1	5' gcaaccgcaggc 3' (51)	5' agatgaccatccggaa 3' (58)	NM_008077
nrsf	5' ccatgcctcg 3' (52)	5' agccaactc 3' (59)	NM_011263

**Human Primers for ChIP assay**

Name of gene	5' sequence	3' sequence	Accession no.
GAD1 promoter chr2q31	5' tgcgttatattatccgcac 3' (60)	5' cacgggtcg 3' (64)	NT005403
GAD1 3' gene chr2q31	5' ggaggcctatgc 3' (61)	5' gggcttgatgg 3' (65)	NT005403
GRIN 2A promoter chr16	5' aactattctggctactc 3' (62)	5' gctgggag 3' (66)	NT010393
SCN2 promoter chr.2q23	5' ctggataagttactga 3' (63)	5' cagacgaca 3' (67)	NT005403